

Appendix A

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2004, 08:34:06 ; Search time 2 Seconds
(without alignments)
3.960 Million cell updates/sec

Title: us-09-997-857-401
Perfect score: 993
Sequence: 1 MPVPALCLILWALAMVTRPAS.....AQOHLRQIQERLHTALPA 198

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 45 seqs, 40002 residues

Total number of hits satisfying chosen parameters: 45

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : rai.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	865	87.1	191	1	US-09-369-247-65
2					Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-09-369-247-65
; Sequence 65, Application US/09369247
; Patent No. 6563992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (25)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (191)
; OTHER INFORMATION: Xaa equals stop translation
US-09-369-247-65

Query Match 87.1%; Score 865; DB 1; Length 191;
Best Local Similarity 93.2%; Pred. No. 2.3e-83;
Matches 177; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
QY 1 MPVPALCLILWALAMVTRPASAPMGPELAQHEELTLPHGTLQALNGVYRTTEGR 60
DB 1 MPVPALCLILWALAMVTRPASAPMGPELAQHEELTLPHGTLQALNGVYRTTEGR 60
QY 61 TKARNSGLYGRITIELLQGEVSRGEGDAQAELRASILETQMEEDILQQAATAEVLGEVA 120
DB 61 TKARNSGLYGRITIELLQGEVSRGEGDAQAELRASILETQMEEDILQQAATAEVLGEVA 120
QY 121 QAKVLRDSVQRLVQLRSAMWLGPAFRFEVLKAHADKQSHILWALTGHVQQRREWVAQ 180
DB 121 QAKVLRDSVQRLVQLRSAMWLGPAFRFEVLKAHADKQSHILWALTGHVQQRREWVAQ 180
QY 181 QHRLRQIQER 190
DB 181 QHRLRQIQER 190